ESTIMATION OF GENETIC PARAMETERS IN SOYBEAN FOR YIELD AND MORPHOLOGICAL CHARACTERS

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ABSTRACT

The present study was carried out to estimate the important genetic parameters such as genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability (h^2), expected genetic advance (GA) and genetic advance as percent of mean (GAM) for nine quantitative traits of soybean (*Glycine max* L). The study was conducted during Kharif 2013 at Agriculture Research Institute (North) Mingora Swat. The field was laid down in randomized complete block design with three replications. The results indicated that PCV was greater than GCV for all traits except oil contents where PCV and GCV were equal. The PCV and GCV values ranged between 24% and 28% for number of pods plant^{-1}, and 4% and 3% for days to maturity, respectively. Highest heritability was observed for oil contents (99%) and lowest heritability were observed for days to pod formation (31%). Most of the parameters exhibited high heritability including 100 seed weight, grain yield ha^{-1} and oil contents (≥85%), while days to pod formation, and pod length revealed moderate heritability. Expected genetic advance ranged between 1.78 (oil contents) and 780.80 (seed yield ha^{-1}), while genetic advance as percent of mean ranged from 36.93 (number of pods plant^{-1}) to 4.76 (days to maturity). Economically important characters including pod numbers plant^{-1}, 100 seed weight and seed yield exhibited high variability and heritability with moderate genetic advance as percent of mean. It can be concluded that these characters may be used as selection tool in future breeding programs.

Keywords: genetic advance, genotypic coefficient of variance, phenotypic coefficient of variance, heritability, quantitative traits, soybean.

INTRODUCTION

Soybean (*Glycine max* L.) of the family Leguminosae, is considered a miracle crop because of its extraordinary qualities. In Pakistan, it is one of the non-conventional oil seed crops that can successfully be grown during Kharif and Rabi season (Arshad *et al.,* 2006). Soybean is the one among the important vegetable food source in the world. This is due to its high content of oil (20%) and protein (40%) in its seed (Conab, 2010). It is grown in East and South East Asia mainly for food, feed and medicinal purposes (Lawrence, 2011). This plant contains about 37-42% of high quality protein, 6% ash, 29% carbohydrate and 17

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to 24% oil, comprising 85% poly un-saturated fatty acids with two essential fatty acids (lenoleic and linolenic acid) (Balasubramaniyan and Palaniappan, 2003). In Pakistan, it is grown on a very small area only in Khyber Pukhtunkwa province. It is commercially grown in 35 countries (OECD, 2000). During 2010-11, 318.57 million metric tons soybean was produced globally on 118.14 million hectares with the average yield of 2700 kg ha^{-1}. USA, Brazil and Argentina are the leading producers both in terms of acreage and its yield per unit area (USDA, 2016). According to Agriculture Statistics of Pakistan, soybean was cultivated on an area of 129 hectares in Pakistan, which produced 89 tons, with 573 kg ha^{-1} yield. The cultivation of soybean drastically reduced during last ten years (Government of Pakistan, 2010-11).

The estimation of genetic and phenotypic parameters like heritability, correlations and expected gains from selection have a prime role in genetic breeding programs. These parameters enable the breeders to make decisions about the appropriate methods to handle the populations and select the characteristics to be considered in initial and advanced steps of the breeding program (Farias, 2008). The continuous improvement of genetic breeding of soybean depends on the information about genetic variability, genetic parameters and their application, that assists the breeders in reliable selection process. Important genetic parameters include heritability, and genetic advance that enable the plant breeders to select the best breeding strategy (Hamawaki *et al.,* 2012). In this backdrop a research study was designed to estimate genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability (h^2), expected genetic advance (GA) and genetic advance as percent of mean (GAM) for yield and morphological traits of soybean that may be used as selection tools in future breeding programs.

MATERIALS AND METHODS

The present study was conducted at Agriculture Research Institute (North) Mingora Swat during the Kharif season of the year 2013. Nineteen different soybean accessions including two checks (Malakand-96 and Swat-84) of diverse genetic background were evaluated. Experiment was laid out in RCBD model with three replications. Each row was 5 m long and was spaced 45 cm apart. Plot size consisted of four rows, each was five meter long and forty-five centimeters apart (5x0.45x4). Sowing was done in the last week of May, 2013. Standard agronomic practices were followed for successful crop production. Fertilizer was applied at the time of sowing @ 25kg N and 60 kg P$_2$O$_5$. Data was recorded for the following parameters after germination; days to 50% flowering (DFF), days to pod formation (DPF), days to maturity (DM), plant height (PH), number of pods plant^{-1} (NPP^{-1}), pod length (PL), 100-seed weight (HSW), seed yield ha^{-1} (SY ha^{-1}), Harvest Index (HI) and oil contents (OC %). The genotypic and phenotypic components of variance were calculated according to formulae given for the observed characters.

$$Genotypic\ Variance\ (Vg) = \frac{GMS-EMS}{r} \qquad 1$$

(Vg: Genotypic Variance, GMS: Genotypic Mean Square and EMS: Error Mean Square, r: replications)

$$Phenotypic\ variance\ (Vp) = Vg + Ve \qquad\qquad 2$$

(Vp: Phenotypic Variance, vg: genotype variance Ve: Environmental variance)
Genotypic and phenotypic coefficients of variability were computed according to Burton and Devane (1953).

$$Genotypic\ coefficient\ of\ variability\ (GCV) = \sqrt{Vg}/\bar{X} \times 100 \qquad 3$$

$$Phenotypic\ coefficient\ of\ variability\ (PCV) = \sqrt{Vp}/\bar{X} \times 100 \qquad 4$$

($\bar{X}$: General mean)

The PCV and GCV values are ranked as low, medium and high (Shivasubramanian and Menon, 1973). Broad sense heritability was estimated based on the ratio of genotypic variance to the phenotypic variance and was expressed in percentage (Hanson *et al.*, 1956). Heritability values are categorized as low, moderate and high (Robinson *et al.*, 1949).

$$Heritability\ (h^2) = \frac{Vg}{Vp} \times 100 \qquad\qquad 5$$

Genetic advance (GA) was computed according to the formula given by Johnson *et al.* (1955). Genetic advance as percent of mean (GAM) expressed in percentage was also computed according to Robinson *et al.* (1949). Genetic advance as percent of mean was classified as low, moderate and high (Johnson *et al.,* 1955).

$$GA = k\sigma p h^2 \qquad\qquad 6$$

(GA: Genetic Advance, k: Selection deferential, σp: Standard deviation and h^2: Heritability)

RESULTS AND DISCUSSION

The coefficient of variance i.e GCV and PCV give information about the nature and magnitude of variation. It clarifies either the variation are due to genetic causes or environmental causes. Usually the PCV is greater than the GCV. If the differences between PCV and GCV are larger then the environmental effects on the character will be more. In the present study, most characters exhibited moderate GCV and PCV with smaller differences, except days to pod formation (Table 1). Heritability gives information about the inheritance of the character. Traits having high heritability are easy to improve through selection. Days to 50% flowering exhibited moderate estimate of PCV (12.48) and GCV (10.86) coupled with high heritability (75.73). Barh *et al.* (2014) reported high heritability for this character in soybean. Abady *et al.* (2013); Ghodrati *et al.* (2013); Gohil *et al.* (2006) and Malik *et al.* (2006) reported moderate PCV and GCV along with high heritability for this trait. It suggests that this character is more due to genetic base with lesser effects of the environment. The high heritability indicates a greater scope for selection to improve this character. Days to pod formation exhibited moderate estimate of PCV (11.68) and low GCV (6.52) with moderate heritability

(31.33). Malik *et al.* (2006a) and Malik *et al.* (2007) revealed moderate values of PCV and GCV. Low value of PCV (3.82) and GCV (3.23) along with high heritability (70.96) was revealed for days to maturity. Gohil *et al.* (2006); Malik *et al.* (2006b); Malik *et al.* (2007); Ghodrati *et al.* (2013); Okonkwo and Idahosa, (2013) and Barh *et al.* (2014), reported low PCV and GCV coupled with high heritability for this character. Abady *et al.* (2013) had also reported high heritability for days to maturity. These findings clarify that this trait is under genetic control and can be improved through selection. High values of PCV (22.45) and GCV (21.42) were shown for the plant height with high heritability (91.07). Abady *et al.* (2013); Dilanesaw *et al.* (2013); Ghodrati *et al.* (2013) and Barh *et al.* (2014) reported high GCV and PCV for plant height. However, Aditya *et al.* (2013), reported moderate GCV and PCV with high heritability for plant height, and Bekele and Getnet, (2011) reported low PCV and GCV with moderate heritability for this character. These findings confirm the genetic base of this trait. It also recommends selection as tool for the improvement of this trait. High PCV (28.43) and GCV (24.48) coupled with high heritability (74.17) were estimated for number of pods plant^{-1}. Gohil *et al.* (2006); Malik *et al.* (2006b); Malik *et al.* (2007); Abady *et al.* (2013); Aditya *et al.* (2013); Dilanesaw *et al.* (2013) and Barh *et al.* (2014) reported high PCV and GCV along with high heritability for pods plant^{-1}. Low PCV (6.53) and GCV (4.40) and moderate heritability (45.40) were observed for pod length. Reni and Rao, (2013) reported moderate GCV and PCV for pod length. These findings confirm the genetic base of this trait. It also recommends selection as tool for the improvement of this trait.

The 100-seed weight revealed moderate values of PCV (17.23) and GCV (13.59) with high heritability (86.34). Gohil *et al.* (2006) reported moderate PCV and GCV coupled with high heritability for this character. However, Aditya *et al.* (2013) reported high GCV and PCV with high heritability for this trait, while Barh *et al.* (2014) and Malik *et al.* (2007) reported high values of PCV and GCV along with high heritability for 100-seed weight. These findings confirm the genetic control of this trait with suggestion of selection as improvement tool for this trait. Seed yield also revealed moderate values for PCV (15.51) and GCV (14.42) with high heritability (84.33). Abady *et al.* (2013) reported high heritability for seed yield plot^{-1}. However, Gohil *et al.* (2006); Malik *et al.* (2006a); Malik *et al.* (2006b); Malik *et al.* (2007); Aditya *et al.* (2013) and Barh *et al.* (2014), reported high GCV and PCV with high heritability for seed yield and reported low values of PCV and GCV along with high heritability for seed yield. These findings reveal that seed yield is controlled by genetic factors and selection can improve it. Low values of GCV (5.78) and PCV (5.78) with high heritability (99.40) were observed for oil contents%. Gohil *et al.* (2006) reported low PCV and GCV coupled with high heritability for oil contents%. Reni and Rao, (2013) reported low GCV and PCV with moderate heritability for oil contents%, while Malik *et al.* (2007) reported low values of PCV and GCV for oil contents. Malik *et al.* (2006a) revealed high heritability with moderate GCV and PCV for oil contents. These results confirm that this character is completely genetic with no effects of environment. Selection is a best strategy for improvement of oil contents.

Table 1. Mean, genotypic variance (V_g), phenotypic variance (V_p), genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability (broad sense h^2), expected genetic advance (GA) and genetic advance as percent of mean (GAM) for 9 quantitative traits of soybean (*Glycine max L.*).

Characters	Mean	V_g	V_p	GCV	PCV	h^2	GA	GAM
Days to 50% flowering	65.105	50.023	66.066	10.86	12.48	75.73	10.79	16.58
Days to pod formation	85.561	31.132	99.996	6.52	11.68	31.33	5.48	6.40
Days to maturity	146.351	22.397	31.562	3.23	3.82	70.96	6.98	4.76
Plant height (cm)	133.656	819.789	900.393	21.42	22.45	91.07	47.91	35.48
Number of pod plant[-1]	144.618	1254.155	1690.699	24.48	28.43	74.17	53.46	36.96
Pod length (cm)	4.035	0.0316	0.0696	4.40	6.535	45.40	0.209	5.17
100-seed weight (g)	17.233	5.487	6.355	13.59	17.233	86.34	3.40	19.72
Seed yield (kg ha^{-1})	3348.417	227750.23	270040.48	14.25	15.51	84.33	786.80	23.49
Oil content %	17.697	1.047	1.048	5.78	5.78	99.40	1.78	10.05

Genetic advance (GA) and genetic advance as percent of mean (GAM) gives information about the expected gain in a specific trait due to selection. Moderate genetic advance as percent of mean (GAM) 16.58% was observed for days to 50% flowering. Genetic advance for this character was 10.79. Balla and Seifeldin (2010) reported moderate GA and low GAM. Bakale *et al.* (2012) observed moderate GAM coupled with low GA for days to flowering. These findings suggest that this trait can be improved by selection. Days to pod formation revealed low GAM (6.40%), while GA was 5.48 for this parameter. Malik *et al.* (2006b) observed low genetic advance for days to pod formation. Days to maturity exhibited low GAM (4.76%) and GA was 6.98. Balla and Seifeldin (2010) reported low GAM. Barh *et al.* (2014) observed low GA for days to maturity. Bakale *et al. (*2012) observed low GAM coupled with low GA for days to maturity. Gohil *et al.* (2006) estimated low GAM for maturity. Plant height expressed high GAM (35.48%). GA for this parameter was 47.91. Barh *et al.* (2014) observed high GA for plant height. Bakale *et al.* (2012) observed high GAM for plant height coupled with moderate GA. Dilnesaw *et al.* (2013) has also reported similar results for this parameter. Gohil *et al.* (2006) observed high GAM for this character. Number of pods plant[-1] revealed higher GAM (36.96%) with the GA (53.46). Balla and Seifeldin (2010) reported high GA. Barh *et al.* (2014) observed high GA for this trait. Dilnesaw *et al.* (2013) has also reported high GAM and GA for this parameter. Gohil *et al.* (2006) reported similar results. Pod length exhibited low GA (0.209) and GAM (5.17). Moderate GAM (19.72%) was estimated for 100-seed weight, while GA was 3.40 for this trait. Barh *et al.* (2014) observed low GA for this trait. Bakale *et al.* (2012) observed moderate GAM coupled with low GA for seed weight. Dilnesaw *et al.* (2013) has also reported low GA for this character. Seed yield revealed high GAM (23.49%). GA for seed yield was 786.80. Balla and Seifeldin (2010) reported high GA coupled with moderate GAM. Dilnesaw *et al.* (2013) has also reported similar results for this seed yield. Oil contents % exhibited moderate GAM (10.05%). GA was 1.78 for oil contents%. Barh *et al.* (2014) observed low GA for this trait. Bakale *et al.* (2012) observed moderate GAM coupled with low GA for oil content %. Gohil *et al.* (2006) estimated moderate GA for this trait.

CONCLUSION

The present results indicated that the phenotypic coefficient of variability was higher than genotypic coefficient of variability for all studied characteristics. This means that these traits are less affected by the environment and are under the genetic control. Most of the studied traits revealed high heritability, expected genetic advance and genetic advance as percent of means. The characters having high heritability and high GAM may be used as selection tool in future breeding programs.

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